



## SEQUENCE LISTING

#7  
<110> PEDERSEN, ANDERS H.  
ANDERSON, KIM V.  
BORNAES, CLAUS

<120> FACTOR VII OR VIIA-LIKE MOLECULES

<130> 31-001100US

<140> 09/782,587  
<141> 2001-02-12

<150> PA 2000 00218  
<151> 2000-02-11

<150> 60/184,036  
<151> 2000-02-22

<150> 60/241,916  
<151> 2000-10-18

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<170> PatentIn Ver. 2.1

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20 25 30

Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp  
35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln  
50 55 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn  
65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly  
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys  
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr  
115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg  
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro  
145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln  
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala  
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu  
195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg  
210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn  
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp  
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr  
260 265 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu  
275 280 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg  
290 295 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser  
305 310 315 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser  
325 330 335

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355 360 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  
370 375 380

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Leu Arg Ala Pro Phe Pro  
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Ala  
1  
aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165  
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
5 10 15  
aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp  
20 25 30  
gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261  
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln  
35 40 45

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50 55 60 65	
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70 75 80	
gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly	405
85 90 95	
tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg	453
100 105 110	
tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro	501
115 120 125	
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn	549
130 135 140 145	
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150 155 160	
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165 170 175	
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180 185 190	
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly	741
195 200 205	
gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val	789
210 215 220 225	
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His	837
230 235 240	
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His	885
245 250 255	
gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu	933
260 265 270	

gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp 275 280 285	981
cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu 290 295 300 305	1029
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acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu 370 375 380 385	1269
tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu 390 395 400	1317
cg <sup>g</sup> g <sup>c</sup> c <sup>c</sup> t <sup>t</sup> c <sup>t</sup> c <sup>c</sup> t <sup>g</sup> a <sup>t</sup> a <sup>a</sup> a <sup>a</sup> Arg Ala Pro Phe Pro	1338
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Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
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Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
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Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
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Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly  
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys  
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr  
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Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg  
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro  
145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln  
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala  
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu  
195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg  
210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn  
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp  
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr  
260 265 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu  
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Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg  
290 295 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser  
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Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser  
325 330 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr  
340 345 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys  
355 360 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  
370 375 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu  
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Leu Arg Ala Pro Phe Pro  
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agaggaacag tgcagtttg aggaagcccc ggagattttc aaagacgctg agccggaccaa 240  
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taagaattgg cggAACCTCA tcgctgtgtc cggcgaacac gatctgtccg agcatgacgg 780  
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<211> 28

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<210> 17

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<212> PRT

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<223> Description of Artificial Sequence: synthetic peptide tag

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